
Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=25; hr=10; min=3; sec=27; ms=951;]

Validated By CRFValidator v 1.0.3

Application No: 10573704 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-10 18:29:22.435 **Finished:** 2008-04-10 18:29:23.701

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 266 ms

Total Warnings: 21
Total Errors: 0

No. of SeqIDs Defined: 21
Actual SeqID Count: 21

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W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
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W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
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Input Set:

Output Set:

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Total Warnings: 21

Total Errors: 0

No. of SeqIDs Defined: 21

Actual SeqID Count: 21

Error code Error Description

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

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<110> Fleury, Sylvain
     Girard, Marc
      Roger, Marie-Gaelle
     Mouz, Nicolas
      Serres, Pierre-Francois
<120> New Soluble and Stabilized Trimeric Form of GP41 Polypeptides
<130> 122481
<140> 10573704
<141> 2008-04-10
<150> PCT/IB2004/002433
<151> 2004-07-29
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                     10
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                          25
          20
                                            30
Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
    35 40 45
Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
                  55
   50
Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
           70 75
65
                                                  80
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Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile

90 95

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn 100 105 110

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala 115 120 125

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu 130 135 140

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Lys Asn Glu Gln
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agaatcctgg	ctgtggaaag	atacctaaag	gatcaacagc	tcctggggat	tgacggtagc	180
agtggaggta	gaggtggatc	caatgctagt	tggagtaata	aatctctgga	acagatttgg	240
aatcacacga	cctggatgga	gtgggacaga	gaaattaaca	attacacaag	cttaatacac	300
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Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr 35 40 45

Leu Lys Asp Gln Gln Leu Leu Gly Ile Asp Gly Ser Ser Gly Gly Arg
50 55 60

Gly Gly Ser Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp 65 70 75 80

Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr 85 90 95

Asn Glu Gln Glu Leu Leu Glu Leu Asp Leu Glu His His His His His 115 120 125

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acceptiggat ccaccictac ciccactect accepticality ccaegeagy entry gitter acceptions accepting acception of the control of the co
                                                                                                                                                                                                                                                                             57
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agaatcctgg ctgtggaaag atacctaaag gatcaacagc tcctggggat ttggggtagc 180
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ctggaacaga tttggaatca cacgacctgg atggagtggg acagagaaat taacaattac 300
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Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr
35 40 45

Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Lys Leu 50 55 60

Ile Ser Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser 65 70 75 80

Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu
85 90 95

Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln
100 105 110

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Asn Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp
 115 120 125
Ala Ser Leu Trp Asn Trp Phe Asn Ile
   130
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         5
                            10
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Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu Glu 50 55 60 Gln Ile Trp Asn His Thr Trp Met Glu Trp Asp Arg Glu Ile Asn 65 70 75 80 Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln 85 90 Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser 100 105 110 Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Asp His His His 115 120 125 His His 130 <210> 18 <211> 128 <212> PRT <213> Artificial Sequence <220> <223> Synthetic <400> 18 Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn 1 5 10 15 Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val 20 25 Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr 35 40 45 Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu Glu 55 60

Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn

75

70

65

Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln 90 Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser 100 105 110 Leu Trp Asn Trp Phe Asn Ile Thr Asn Asp His His His His His 115 120 125 <210> 19 <211> 136 <212> PRT <213> Artificial Sequence <220> <223> Synthetic <400> 19 Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn 1 5 10 15 Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val 25 30 20 Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr 40 45 35 Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Gly Arg 55 60 50 Gly Gly Ser Ser Leu Glu Gln Ile Trp Asn His Thr Trp Met Glu 70 75 65 Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu 100 105 110 Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp

115 120 125

130 135

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Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val 20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr 35 40 45

Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Gly Arg
50 55 60

Gly Gly Ser Ser Leu Glu Gln Ile Trp Asn His Thr Trp Met Glu 65 70 75 80

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile 85 90 95

Glu Glu Ser Gl
n Asn Gl
n Glu Lys Asn Glu Glu Leu Leu Glu 100 105 110

Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Asp 115 120 125

His His His His His His 130

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<211> 115

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<213> Artificial Sequence

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<223> Synthetic

Met Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr
1 5 10 15

Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Tyr Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu 35 40 45

Glu Gln Ile Trp Asn His Thr Trp Met Glu Trp Asp Arg Glu Ile
50 55 60

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn 65 70 75 80

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala 85 90 95

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Asp His His His 100 105 110

His His His

115